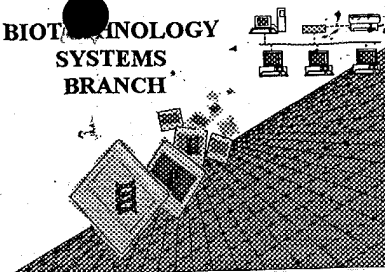


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/819,667A  
Source: OIRE  
Date Processed by STIC: 7/31/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/819,667A

TIME: 14:45:03

Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt

Output Set: N:\CRF3\07312001\I819667A.raw

2 <110> APPLICANT: CANON INC.  
 4 <120> TITLE OF INVENTION: Nucleic Acid Fragment Primer or Probe, and Method of  
 5 Detecting Polyhydroxyalkanoate Synthesizing Microorganism by  
 6 Using the Same  
 8 <130> FILE REFERENCE: 4052014  
 9 -> 10 <140> CURRENT APPLICATION NUMBER: US/09/819,667A  
 10 <141> CURRENT FILING DATE: 2001-03-29  
 E--> 10 <160> NUMBER OF SEQ ID NOS: 9  
 12 <170> SOFTWARE: Microsoft Word

Does Not Comply  
 Corrected Diskette Needed

## ERRORED SEQUENCES

100 <210> SEQ ID NO: 9  
 101 <211> LENGTH: 30 25  
 102 <212> TYPE: DNA  
 103 <213> ORGANISM: Artificial Sequence  
 105 <220> FEATURE:  
 106 <223> OTHER INFORMATION: Primer for PCR multiplication  
 108 <400> SEQUENCE: 9  
 E--> 109 ccaac agcgg bcayr tscag agcat 25  
 199 <210> SEQ ID NO: 18  
 200 <211> LENGTH: 30 25 last sequence in file  
 201 <212> TYPE: DNA  
 202 <213> ORGANISM: Artificial Sequence  
 204 <220> FEATURE:  
 205 <223> OTHER INFORMATION: Primer for PCR multiplication  
 207 <400> SEQUENCE: 18  
 208 ccaac agcgg gcatg tccag agcat 25  
 E--> 212 hy\_main 157155 v 1

Per 1.822 of sequence rules,  
 group all  
 non-coding bases  
 into groups of 10  
 group all bases  
 into 10's  
 (non-coding bases)  
 delete at end of file

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/819,667A

DATE: 07/31/2001

TIME: 14:45:04

Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt

Output Set: N:\CRF3\07312001\I819667A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier ✓  
L:109 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:25 SEQ:9 ✓  
L:212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:33 SEQ:18  
L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:212 M:112 C: (48) String data converted to lower case,  
L:212 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:33 SEQ:18  
L:10 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (9) Counted (18)